ƒ5

PCT09

```
      RAW SEQUENCE LISTING              DATE: 01/23/2002
      PATENT APPLICATION:  US/09/830,980    TIME: 17:42:46

      Input Set : A:\55871745.app
      Output Set: N:\CRF3\01232002\I830980.raw
```

ρ5

ρ

```
 3 <110> APPLICANT: COHEN, STEPHEN
 4        BOUWMEESTER, ANTONIUS
 5        ROYET, JULIEN
 7 <120> TITLE OF INVENTION: REGULATOR OF NOTCH SIGNALING ACTIVITY
 9 <130> FILE REFERENCE: 55880(71745)
11 <140> CURRENT APPLICATION NUMBER: 09/830,980
12 <141> CURRENT FILING DATE: 2001-05-02
14 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01891
15 <151> PRIOR FILING DATE: 1999-11-03
17 <150> PRIOR APPLICATION NUMBER: GB 9824045.0
18 <151> PRIOR FILING DATE: 1998-11-03
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 480
26 <212> TYPE: PRT
27 <213> ORGANISM: Drosophila sp.
29 <400> SEQUENCE: 1
```

ENTERED

```
30 Met Gln Glu Thr Asp Thr Glu Gln Glu Ala Thr Pro His Thr Ile Gln
31  1               5                  10                  15
33 Ala Arg Leu Val Tyr Thr Gly Glu Glu Ala Gly Pro Pro Ile Asp Leu
34              20                  25                  30
36 Pro Ala Gly Ile Thr Thr Gln Gln Leu Gly Leu Ile Cys Asn Ala Leu
37          35                  40                  45
39 Leu Lys Asn Glu Glu Ala Thr Pro Tyr Leu Phe Phe Val Gly Glu Asp
40      50                  55                  60
42 Glu Ile Lys Lys Ser Leu Glu Asp Thr Leu Asp Leu Ala Ser Val Asp
43 65                  70                  75                  80
45 Thr Glu Asn Val Ile Asp Ile Val Tyr Gln Pro Gln Ala Val Phe Lys
46                  85                  90                  95
48 Val Arg Pro Val Thr Arg Cys Thr Ser Ser Met Pro Gly His Ala Glu
49          100                 105                 110
51 Ala Val Val Ser Leu Asn Phe Ser Pro Asp Gly Ala His Leu Ala Ser
52          115                 120                 125
54 Gly Ser Gly Asp Thr Thr Val Arg Leu Trp Asp Leu Asn Thr Glu Thr
55      130                 135                 140
57 Pro His Phe Thr Cys Thr Gly His Lys Gln Trp Val Leu Cys Val Ser
58 145                 150                 155                 160
60 Trp Ala Pro Asp Gly Lys Arg Leu Ala Ser Gly Cys Lys Ala Gly Ser
61              165                 170                 175
63 Ile Ile Ile Trp Asp Pro Glu Thr Gly Gln Gln Lys Gly Arg Pro Leu
64          180                 185                 190
66 Ser Gly His Lys Lys His Ile Asn Cys Leu Ala Trp Glu Pro Tyr His
```

RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/830,980   TIME: 17:42:46

Input Set : A:\55871745.app
Output Set: N:\CRF3\01232002\I830980.raw

```
67           195                200                205
69 Arg Asp Pro Glu Cys Arg Lys Leu Ala Ser Ala Ser Gly Asp Gly Asp
70     210                215                220
72 Cys Arg Ile Trp Asp Val Lys Leu Gly Gln Cys Leu Met Asn Ile Ala
73 225                230                235                240
75 Gly His Thr Asn Ala Val Thr Ala Val Arg Trp Gly Gly Ala Gly Leu
76             245                250                255
78 Ile Tyr Thr Ser Ser Lys Asp Arg Thr Val Lys Met Trp Arg Ala Ala
79             260                265                270
81 Asp Gly Ile Leu Cys Arg Thr Phe Ser Gly His Ala His Trp Val Asn
82         275                280                285
84 Asn Ile Ala Leu Ser Thr Asp Tyr Val Leu Arg Thr Gly Pro Phe His
85     290                295                300
87 Pro Val Lys Asp Arg Ser Lys Ser His Leu Ser Leu Ser Thr Glu Glu
88 305                310                315                320
90 Leu Gln Glu Ser Ala Leu Lys Arg Tyr Gln Ala Val Cys Pro Asp Glu
91             325                330                335
93 Val Glu Ser Leu Val Ser Cys Ser Asp Asp Asn Thr Leu Tyr Leu Trp
94             340                345                350
96 Arg Asn Asn Gln Asn Lys Cys Val Glu Arg Met Thr Gly His Gln Asn
97         355                360                365
99 Val Val Asn Asp Val Lys Tyr Ser Pro Asp Val Lys Leu Ile Ala Ser
100     370                375                380
102 Ala Ser Phe Asp Lys Ser Val Arg Leu Trp Arg Ala Ser Asp Gly Gln
103 385                390                395                400
105 Tyr Met Ala Thr Phe Arg Gly His Val Gln Ala Val Tyr Thr Val Ala
106             405                410                415
108 Trp Ser Ala Asp Ser Arg Leu Ile Val Ser Gly Ser Lys Asp Ser Thr
109         420                425                430
111 Leu Lys Val Trp Ser Val Gln Thr Lys Lys Leu Ala Gln Glu Leu Pro
112     435                440                445
114 Gly His Ala Asp Glu Val Phe Gly Val Asp Trp Ala Pro Asp Gly Ser
115     450                455                460
117 Arg Val Ala Ser Gly Gly Lys Asp Lys Val Ile Lys Leu Trp Ala Tyr
118 465                470                475                480
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 1555
124 <212> TYPE: DNA
125 <213> ORGANISM: Drosophila sp.
127 <400> SEQUENCE: 2
128 aattcccaaa aaatgcagga gacggacacg gagcaagagg ccacgccaca tacgatacag 60
129 gcgcgcctcg tttacacggg cgaggaagcc ggcccgccaa tcgacctgcc ggcaggaatc 120
130 actacccagc aattgggact gatttgcaac gcgctgctga aaaacgagga agccactcca 180
131 tatttgtttt tcgtgggcga ggatgagatc aagaagagcc tggaggacac gttggacttg 240
132 gcgtcagtgg acaccgaaaa cgtgatcgat attgtgtatc agccacaggc ggttttcaaa 300
133 gtgcgcccag tgacaagatg cacgagttcc atgccgggac acgccgaggc tgtggtttcg 360
134 ctgaatttca gcccggatgg tgctcatctc gccagtggaa gtggcgacac cacagtgcga 420
135 ttgtgggatc ttaacacaga gacaccgcac ttcacctgca caggtcataa gcagtgggtt 480
136 ctgtgcgtat cctgggctcc ggatggcaaa cggttggcca gcggttgcaa agcgggctct 540
```

```
137 ataatcatct gggacccgga gacgggtcag cagaaggggc gacccttgag tgggcacaag 600
138 aaacacatca actgcctcgc ctgggaaccg tatcatcgcg atccggagtg caggaaactt 660
139 gcttccgcca gtggagacgg ggactgccgg atttgggacg taaaattggg ccagtgcctt 720
140 atgaacattg ccggacacac aaatgctgtg acagcagtga gatgggggtgg agcgggcctt 780
141 atttatacat cctccaaaga tcgcacagtg aagatgtggc gagcagctga tggaatcttg 840
142 tgccggacgt tctctggcca agctcactgg gtaaacaaca ttgcgctgag caccgattac 900
143 gtcctgcgca ctggtccatt ccatccggtg aaggatcgct ccaagagcca cctcagtttg 960
144 agcactgagg aattgcagga atctgccttg aagcgctacc aggccgtgtg ccctgacgag 1020
145 gtggagtcgc tggtttcctg ttcggatgac aacaccctct atctgtggcg gaacaaccag 1080
146 aacaagtgcg ttgagcgcat gacagggcac cagaacgtgg tcaacgatgt gaaatattcg 1140
147 ccggatgtaa agctaattgc gtctgcttca tttgacaagt cagtgcgtct gtggcgagcc 1200
148 agcgatggtc agtacatggc caccttccgg ggtcatgtgc aggctgttta cacggttgcc 1260
149 tggtccgcgg actcccgctt gattgtttcc ggcagcaaag actcaactct aaaagtatgg 1320
150 agtgtgcaga cgaagaaact ggcacaggag ctgcctggac atgcggatga ggtgttcgga 1380
151 gtggactggg cgcccgatgg ctctagagtt gcctctggtg gcaaggacaa agttataaag 1440
152 ctatgggctt attaacaaat cattaacttg tacacggtaa gaaaatactt aggaataaag 1500
153 taaaacgtcc tgagtaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa      1555
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 513
158 <212> TYPE: PRT
159 <213> ORGANISM: Saccharomyces cerevisiae
161 <400> SEQUENCE: 3
162 Met Ser Thr Leu Ile Pro Pro Pro Ser Lys Lys Gln Lys Lys Glu Ala
163  1               5                  10                  15
165 Gln Leu Pro Arg Glu Val Ala Ile Ile Pro Lys Asp Leu Pro Asn Val
166              20                  25                  30
168 Ser Ile Lys Phe Gln Ala Leu Asp Thr Gly Asp Asn Val Gly Gly Ala
169          35                  40                  45
171 Leu Arg Val Pro Gly Ala Ile Ser Glu Lys Gln Leu Glu Glu Leu Leu
172      50                  55                  60
174 Asn Gln Leu Asn Gly Thr Ser Asp Asp Pro Val Pro Tyr Thr Phe Ser
175  65                  70                  75                  80
177 Cys Thr Ile Gln Gly Lys Lys Ala Ser Asp Pro Val Lys Thr Ile Asp
178              85                  90                  95
180 Ile Thr Asp Asn Leu Tyr Ser Ser Leu Ile Lys Pro Gly Tyr Asn Ser
181             100                 105                 110
183 Thr Glu Asp Gln Ile Thr Leu Leu Tyr Thr Pro Arg Ala Val Phe Lys
184             115                 120                 125
186 Val Lys Pro Val Thr Arg Ser Ser Ser Ala Ile Ala Gly His Gly Ser
187         130                 135                 140
189 Thr Ile Leu Cys Ser Ala Phe Ala Pro His Thr Ser Ser Arg Met Val
190 145                 150                 155                 160
192 Thr Gly Ala Gly Asp Asn Thr Ala Arg Ile Trp Asp Cys Asp Thr Gln
193             165                 170                 175
195 Thr Pro Met His Thr Leu Lys Gly His Tyr Asn Trp Val Leu Cys Val
196             180                 185                 190
198 Ser Trp Ser Pro Asp Gly Glu Val Ile Ala Thr Gly Ser Met Asp Asn
199         195                 200                 205
201 Thr Ile Arg Leu Trp Asp Pro Lys Ser Gly Gln Cys Leu Gly Asp Ala
```

RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/830,980   TIME: 17:42:46

Input Set : A:\55871745.app
Output Set: N:\CRF3\01232002\I830980.raw

```
202    210                   215              220
204 Leu Arg Gly His Ser Lys Trp Ile Thr Ser Leu Ser Trp Glu Pro Ile
205 225              230              235              240
207 Leu Val Lys Pro Gly Ser Lys Pro Arg Leu Ala Ser Ser Ser Lys Asp
208              245              250              255
210 Gly Thr Ile Lys Ile Trp Asp Thr Val Ser Arg Val Cys Gln Tyr Thr
211          260              265              270
213 Met Ser Gly His Thr Asn Ser Val Ser Cys Val Lys Trp Gly Gly Gln
214          275              280              285
216 Gly Leu Leu Tyr Ser Gly Ser His Asp Arg Thr Val Arg Val Trp Asp
217     290              295              300
219 Ile Asn Ser Gln Gly Arg Cys Ile Asn Ile Leu Lys Ser His Ala His
220 305              310              315              320
222 Trp Val Asn His Leu Ser Leu Ser Thr Asp Tyr Ala Leu Arg Ile Gly
223              325              330              335
225 Ala Phe Asp His Thr Gly Lys Lys Pro Ser Thr Pro Glu Glu Ala Gln
226          340              345              350
228 Lys Lys Ala Leu Glu Asn Tyr Glu Lys Ile Cys Lys Lys Asn Gly Asn
229          355              360              365
231 Ser Glu Glu Met Met Val Thr Ala Ser Asp Asp Tyr Thr Met Phe Leu
232     370              375              380
234 Trp Asn Pro Leu Lys Ser Thr Lys Pro Ile Ala Arg Met Thr Gly His
235 385              390              395              400
237 Gln Lys Leu Val Asn His Val Ala Phe Ser Pro Asp Gly Arg Tyr Ile
238              405              410              415
240 Val Ser Ala Ser Phe Asp Asn Ser Ile Lys Leu Trp Asp Gly Arg Asp
241          420              425              430
243 Gly Lys Phe Ile Ser Thr Phe Arg Gly His Ile Ala Ser Val Tyr Gln
244          435              440              445
246 Val Ala Trp Ser Ser Asp Cys Arg Leu Leu Val Ser Cys Ser Lys Asp
247     450              455              460
249 Thr Thr Leu Lys Val Trp Asp Val Arg Thr Arg Lys Leu Ser Val Asp
250 465              470              475              480
252 Leu Pro Gly Ile Lys Thr Lys Leu Tyr Val Asp Trp Ser Val Asp Gly
253          485              490              495
255 Lys Arg Val Cys Ser Gly Gly Lys Asp Lys Met Val Arg Leu Trp Thr
256          500              505              510
258 His
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 351
264 <212> TYPE: PRT
265 <213> ORGANISM: Codonanthe elegans
267 <220> FEATURE:
268 <221> NAME/KEY: MOD_RES
269 <222> LOCATION: (184)..(185)
270 <223> OTHER INFORMATION: Variable amino acid
272 <400> SEQUENCE: 4
273 Pro Gln Ile Ser Val Ser Glu Asp Glu Asn Glu Leu Gly Gly Ser Gly
274   1             5               10               15
```

RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/830,980   TIME: 17:42:46

Input Set : A:\55871745.app
Output Set: N:\CRF3\01232002\I830980.raw

```
276 Ile Leu Val Pro Val Asp Ile Ser Thr Asn Glu Leu Gln Ile Leu Cys
277             20              25              30
279 Asn Gln Leu Leu Gly Ser Arg Phe Cys Leu Asn Asn Glu Phe Ser Val
280         35              40              45
282 Ser Gly Ala Glu Ile Val Asp Ser Ile Arg Lys Ser Leu Glu Glu Ile
283         50              55              60
285 Asp Phe Glu Thr Leu Lys Leu Val Tyr Gln Pro Gln Ala Val Phe Arg
286  65              70              75              80
288 Val Arg Pro Val Thr Arg Cys Ser Ala Ser Ile Pro Gly His Gly Glu
289             85              90              95
291 Pro Val Ile Ser Ala Gln Phe Ser Pro Asp Gly Arg Gly Leu Ala Ser
292             100             105             110
294 Gly Ser Gly Asp Gln Thr Met Arg Ile Trp Asp Ile Glu Leu Glu Leu
295         115             120             125
297 Pro Leu His Thr Cys Lys Ser His Lys Ser Trp Val Leu Cys Ile Ala
298     130             135             140
300 Trp Ser Pro Asp Ala Thr Lys Ile Ala Ser Ala Cys Lys Asn Gly Glu
301 145             150             155             160
303 Ile Cys Ile Trp Asn Ala Lys Thr Gly Glu Gln Ile Gly Lys Thr Leu
304             165             170             175
306 Lys Arg His Lys Gln Trp Ile Xaa Xaa Leu Ala Trp Gln Pro Thr Val
307         180             185             190
309 Lys Met Trp Arg Ala Asp Asp Gly Val Met Cys Arg Asn Met Thr Gly
310         195             200             205
312 His Ala His Trp Ile Asn Thr Leu Ala Leu Asn Thr Asp Tyr Ala Leu
313     210             215             220
315 Arg Thr Ser Cys Phe Glu Pro Ser Lys Ile Asn Arg Met Thr Gly His
316 225             230             235             240
318 Met Gln Leu Val Asn Gln Val Val Phe Ser Pro Asp Thr Arg Tyr Ala
319             245             250             255
321 Ser Ala Ser Phe Asp Lys Ser Val Lys Leu Trp Cys Gly Arg Thr Gly
322         260             265             270
324 Lys Tyr Leu Ala Ser Phe Arg Gly His Val Gly Pro Val Tyr Gln Val
325         275             280             285
327 Ala Trp Ser Ala Asp Ser Arg Leu Leu Val Ser Gly Ser Ala Asp Ser
328     290             295             300
330 Thr Leu Lys Val Phe Glu Leu Lys Thr Lys Ser Leu Tyr Tyr Asp Leu
331 305             310             315             320
333 Pro Gly His Gly Asp Glu Val Phe Thr Val Asp Trp Ser Pro Glu Gly
334             325             330             335
336 Thr Lys Val Val Ser Gly Gly Lys Asp Lys Val Leu Lys Leu Trp
337             340             345             350
340 <210> SEQ ID NO: 5
341 <211> LENGTH: 103
342 <212> TYPE: PRT
343 <213> ORGANISM: Mus sp.
345 <220> FEATURE:
346 <221> NAME/KEY: MOD_RES
347 <222> LOCATION: (39)
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 01/23/2002
PATENT APPLICATION: **US/09/830,980**   TIME: 17:42:47

Input Set : **A:\55871745.app**
Output Set: **N:\CRF3\01232002\I830980.raw**

```
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
```